ABSTRACT

The invention provides methods for the prediction of an epitope in a target protein. An epitope of the target protein can be bound by a given molecule, *e.g.*, by an antibody. In particular, the methods of the invention comprise (i) identifying a plurality of cross-reactive proteins, *i.e.*, proteins that can be bound by the same molecule, *e.g.*, by the same antibody, as the target protein using, *e.g.*, protein microarrays; and (ii) comparing the amino acid sequences of the target protein and the cross-reactive proteins with each other to identify windows of sequence homology, wherein the windows of sequence homology correspond to the epitope.

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